3. DNA

Program Name: DNA.java   Input File: dna.dat

You are taking an intro biology class, and your first homework is to check whether two equal length DNA strands are "good". In other words, a pair of good strings only consists of the letters A, T, G and C, and for each position in the strand, an A in one of the strings must matched to a T in the other string, or a G matched to a C. This seems pretty easy at first, but as you get going on your homework, you realize the teacher has given you some pretty long strings! Since you would rather not spend forever on the homework, you decide to write a program that analyzes these DNA string pairs for you.

Input
The first line will be a single integer T, the number of problems on your homework. It will be followed by T pairs of lines. Each line will contain a single string representing a DNA strand.

Output
For each problem, output "GOOD" if the string pairs match properly as described above, or "BAD" if there is at least one non-matching pair of characters.

Example Input File
```
3
ATGC
TACG
ATGC
CGTA
AGQ
TCF
```

Example Output to Screen
```
GOOD
BAD
BAD
```

Explanation:
In the first case, the character pairs at all 4 index positions are valid, so the answer is good.
In the second case, the first pair, A-C is not a valid matching, so the answer is bad.
In the third case, the last pair, Q-F, is not valid, so the answer is bad.